



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Coughlin, Shaun  
Ishihari, Hiroaki  
Connolly, Andrew
- (ii) TITLE OF THE INVENTION: Protease Activated Receptor  
3 and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: MORRISON & FOERSTER  
(B) STREET: 755 Page Mill Road  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/208,629  
(B) FILING DATE: 08-DEC-1998  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/742,440  
(B) FILING DATE: 30-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Catherine M. Polizzi  
(B) REGISTRATION NUMBER: 40,130  
(C) REFERENCE/DOCKET NUMBER: 220002060310
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (650) 813-5600  
(B) TELEFAX: (650) 494-0792  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| TGACTTTGTA | TACTTAACAA | CATCCTGTAG | CCGGGTCTCA | GGACATCAAG | ATGAAAATCC | 60   |
| TTATCTTGGT | TGCAGCTGGG | CTGCTGTTTC | TGCCAGTCAC | TGTTTGCCAA | AGTGGCATAA | 120  |
| ATGTTTCAGA | CAACTCAGCA | AAGCCAACCT | TAACATTATA | GAGTTTTAAT | GGGGGTCCCC | 180  |
| AAAATACCTT | TGAAGAATTC | CCACTTTCTG | ACATAGAGGG | CTGGACAGGA | GCCACCACAA | 240  |
| CTATAAAAGC | GGAGTGTCCT | GAGGACAGTA | TTTCAACTCT | CCACGTGAAT | AATGCTACCA | 300  |
| TAGGATACCT | GAGAAGTTCC | TTAAGTACCC | AAGTGATACC | TGCCATCTAT | ATCCTGCTGT | 360  |
| TTGTGGTTGG | TGTACCATCC | AACATCGTGA | CCCTGTGGAA | ACTCTCCTTA | AGGACCAAAT | 420  |
| CCATCAGTCT | GGTCATCTTT | CACACCAACC | TGGCCATCGC | AGATCTCCTT | TTCTGTGTCA | 480  |
| CACTGCCATT | TAAGATCGCC | TACCATCTCA | ATGGCAACAA | CTGGGTATTT | GGCGAGGTCA | 540  |
| TGTGCCGGAT | CACCACGGTC | GTTTTCTACG | GCAACATGTA | CTGCGCTATC | CTGATCCTCA | 600  |
| CTTGATGGG  | CATCAACCGC | TACCTGGCCA | CGGCTCACCC | TTTCACATAC | CAGAAGCTGC | 660  |
| CCAAACGCAG | CTTCTCCTTG | CTCATGTGTG | GCATAGTGTG | GGTCATGGTT | TTCTTATACA | 720  |
| TGCTGCCCTT | TGTCATCCTG | AAGCAGGAGT | ACCACCTCGT | CCACTCAGAG | ATCACCACCT | 780  |
| GCCACGATGT | CGTCGACGCG | TCCGAGTCCC | CATCATCCTT | CCGATTCTAC | TACTTCGTCT | 840  |
| CCTTAGCATT | CTTTGGGTTC | CTCATCCCGT | TTGTGATCAT | CATCTTCTGT | TACACGACTC | 900  |
| TCATCCACAA | ACTTAAATCA | AAGGATCGGA | TATGGCTGGG | CTACATCAAG | GCCGTCCTCC | 960  |
| TCATCCTTGT | GATTTTCACA | ATTGCTTTTG | CCCCACCAA  | CATCATACTC | GTAATCCACC | 1020 |
| ATGCCAACTA | CTACTACCAC | AATACCGACA | GCTTGTAATT | TATGTATCTT | ATTGCTCTGT | 1080 |
| GCCTGGGGAG | CCTGAATAGC | TGCCTAGATC | CATTCCCTTA | CTTTGTCTAT | TCGAAAGTTG | 1140 |
| TAGATCAGCT | TAATCCTTAG | TCGGCAATGG | CAAGACCACT | TTAGAGACCA | AGGAGAGATA | 1200 |
| TCTGGGAAGA | CATACATGCT | TGGC       |            |            |            | 1224 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1124  
(D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CCATATGCTA | ATATTTCTTT | TCAATTACAG | GCATAAATGT | TTCAGACAAC | TCAGCAAAGC | 60  |
| CAACCTTAAC | TATTAAGAGT | TTTAATGGGG | GTCCCCAAAA | TACCTTTGAA | GAATTCNNNN | 120 |
| NNNTACAAC  | CTCCATGTGA | ATAATGCTAC | CATGGGATAC | CTGAGAAGTT | CCTTAAGTAC | 180 |
| CAAAGTGATA | CCTGCCATCT | ACATCCTGGT | GTTTGTGATT | GGTGTACCAG | CGAACATCGT | 240 |
| GACCTGTGG  | AAACTCTCCT | CAAGGACCAA | ATCCATCTGT | CTGGTCATCT | TTACACCAA  | 300 |
| CCTGGCCATC | GCGGATCTCC | TTTTCTGTGT | CACGCTGCGG | TTTAAGATCN | NCCTACCATC | 360 |
| TCAATGGCAA | CAACTGGGTA | TTTGGCGAGG | TCATGTGCGG | GATCACCACG | GTCGTTTTCT | 420 |
| ACGGCAACAT | GTAATGCGCT | ANNNTCCTGA | TCCTCACCTG | CATGGGCATC | AACCGCTACC | 480 |
| TGGCCACGGC | TCACCTTTTC | ACATACCAGA | AGCTGCCCAA | ACGCAGCTTC | TCCATGCTCA | 540 |
| TGTGTGGCAT | GGTGTGGGCT | ATGGTTTTCT | TATACATGCT | GCCCTTTGTC | ATCCNNNAAG | 600 |
| CAGGAGTACC | ACCTCGTCCA | CTCCGAGATC | ACCACCTGCC | ACGATGTCGT | CGACGCGTGC | 660 |
| GANTCCCCAT | CATCCTTCCG | ATTCTACTAC | TTGCTCTCCT | TAGCATTCTT | TGGGTTCTCT | 720 |
| ATCCCGTTTG | TGATCATCAT | CTTCTGTTAC | ACGACTCTCA | TCCACAAACT | TAAATCAAAA | 780 |
| GATCNGATAT | GGCTGGGCTA | CATCAAGGCC | GTCCTCTCTA | TCCTTGTTGA | TTTACCATC  | 840 |
| TGCTTCCCCC | CCACCAAGNN | NNNGATATC  | TGGGAAGACG | TACATGCTTG | GCTGACTTGT | 900 |
| GCATGGCACC | ATCAGCTCAA | TTTTTAATTT | TTTAATTTTA | ATTTAATTTA | ATTTTATGTT | 960 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| TTTGAGACAG | AGCCTCACTG | TGTAGTCCTG | GCTGGCCTGG | CTGGTTCTCT | ATTTAGACCA | 1020 |
| GGTTAGCCTT | GAAGTCACAG | AGATCTGCCT | GCTTCTGCCT | CCCAAGTGCT | GGGTTCAACC | 1080 |
| AGGTCTGGCA | AGCGCTCCAT | TTTTCAGCTC | CTCTGCAACA | GTGC       |            | 1124 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Leu Tyr Thr

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| TGCTCCATGA | TTTTACAGAT | TTCATAACGT  | TTAAGAGACG | GGACTCAGGT | CATCAAAATG | 60   |
| AAAGCCCTCA | TCTTTGCAGC | TGCTGGCCTC  | CTGCTTCTGT | TGCCCACCTT | TTGTCAGAGT | 120  |
| GGCATGGAAA | ATGATACAAA | CAACTTGGCA  | AAGCCAACCT | TACCCATTAA | GACCTTTCGT | 180  |
| GGAGCTCCCC | CAAATTCTTT | TGAAGAGTTC  | CCCTTTTCTG | CCTTGGAAGG | CTGGACAGGA | 240  |
| GCCACGATTA | CTGTAAAAAT | TAAGTGCCCT  | GAAGAAAGTG | CTTCACATCT | CCATGTGAAA | 300  |
| AATGCTACCA | TGGGGTACCT | GACCAGCTCC  | TTAAGTACTA | AACTGATACC | TGCCATCTAC | 360  |
| CTCCTGGTGT | TTGTAGTTGG | TGTCCC GGCC | AATGCTGTGA | CCCTGTGGAT | GCTTTTCTTC | 420  |
| AGGACCAGAT | CCATCTGTAC | CACTGTATTG  | TACACCAACC | TGGCCATTGC | AGATTTTCTT | 480  |
| TTTTGTGTTA | CATTGCCCTT | TAAGATAGCT  | TATCATCTCA | ATGGGAACAA | CTGGGTATTT | 540  |
| GGAGAGGTCC | TGTGCCGGGC | CACCACAGTC  | ATCTTCTATG | GCAACATGTA | CTGCTCCATT | 600  |
| CTGCTCCTTG | CCTGCATCAG | CATCAACCGC  | TACCTGGCCA | TCGTCCATCC | TTTACCTAC  | 660  |
| CGGGGCCTGC | CCAAGCACAC | CTATGCCTTG  | GTAACATGTG | GACTGGTGTG | GGCAACAGTT | 720  |
| TTCTTATATA | TGCTGCCATT | TTTCATACTG  | AAGCAGGAAT | ATTATCTTGT | TCAGCCAGAC | 780  |
| ATCACCACCT | GCCATGATGT | TCACAACACT  | TGCGAGTCCT | CATCTCCCTT | CCAACTCTAT | 840  |
| TACTTCATCT | CCTTGGCATT | CTTTGGATTG  | TTAATTCCAT | TTGTGCTTAT | CATCTACTGC | 900  |
| TATGCAGCCA | TCATCCGGAC | ACTTAATGCA  | TACGATCATA | GATGGTTGTG | GTATGTAAAG | 960  |
| GCGAGTCTCC | TCATCCTTGT | GATTTTTTACC | ATTGCTTTTG | CTCCAAGCAA | TATTATTCTT | 1020 |
| ATTATTCAAC | ATGCTAACTA | CTACTACAAC  | AACACTGATG | GCTTATATTT | TATATATCTC | 1080 |
| ATAGCTTTGT | GCCTGGGTAG | TCTTAATAGT  | TGCTTAGATC | CATTCCTTTA | TTTTCTCATG | 1140 |
| TCAAAAACCA | GAAATCACTC | CACTGCTTAC  | CTTACAAAAT | AGTGAAATGA | TCTTAGAGAA | 1200 |
| CAAGGACAGC | CATCACAGAG | AACG        |            |            |            | 1224 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|            |            |             |            |             |             |      |
|------------|------------|-------------|------------|-------------|-------------|------|
| ACAGGCATGG | AAAATGATAC | AAACAACCTTG | GCAAAGCCAA | CCTTACCCAT  | TAAGACCTTT  | 60   |
| CGTGGAGCTC | CCCCAAATTC | TTTTGAAGAG  | TTCCCCTTTT | CTGCCTTGGA  | AGGCTGGACA  | 120  |
| GGAGCCACGA | TTACTGTAAA | AATTAAGTGC  | CCTGAAGAAA | GTGCTTCACA  | TCTCCATGTG  | 180  |
| AAAAATGCTA | CCATGGGGTA | CCTGACCAGC  | TCCTTAAGTA | CTAAACTGAT  | ACCTGCCATC  | 240  |
| TACCTCCTGG | TGTTTGTAGT | TGGTGTCCCG  | GCCAATGCTG | TGACCCTGTG  | GATGCTTTTC  | 300  |
| TTCAGGACCA | GATCCATCTG | TACCACTGTA  | TTCTACACCA | ACCTGGCCAT  | TGCAGATTTT  | 360  |
| CTTTTTTGTG | TTACATTGCC | CTTTAAGATA  | GCTTATCATC | TCAATGGGAA  | CAACTGGGTA  | 420  |
| TTTGGAGAGG | TCCTGTGCCG | GGCCACCACA  | GTCATCTTCT | ATGGCAACAT  | GTACTGCTCC  | 480  |
| ATTCTGCTCC | TTGCCTGCAT | CAGCATCAAC  | CGCTACCTGG | CCATCGTCCA  | TCCTTTCACC  | 540  |
| TACCGGGGCC | TGCCCAAGCA | CACCTATGCC  | TTGGTAACAT | GTGGACTGGT  | GTGGGCAACA  | 600  |
| GTTTTCTTAT | ATATGCTGCC | ATTTTTCATA  | CTGAAGCAGG | AATATTATCT  | TGTTCAGCCA  | 660  |
| GACATCACCA | CCTGCCATGA | TGTTCACAAAC | ACTTGCGAGT | CCTCATCTCC  | CTTCCAACCTC | 720  |
| TATTACTTCA | TCTCCTTGGC | ATTCTTTGGA  | TTCTTAATTC | CATTTGTGCT  | TATCATCTAC  | 780  |
| TGCTATGCAG | CCATCATCCG | GACACTTAAT  | GCATACGATC | ATAGATGGTT  | GTGGTATGTT  | 840  |
| AAGGCGAGTC | TCCTCATCCT | TGTGATTTTT  | ACCATTGTCT | TTGCTCCAAG  | CAATATTATT  | 900  |
| CTTATTATTC | ACCATGCTAA | CTACTACTAC  | AACAACACTG | ATGGCTTATA  | TTTTATATAT  | 960  |
| CTCATAGCTT | TGTGCCTGGG | TAGTCTTAAT  | AGTTGCTTAG | ATCCATTTCCT | TTATTTTCTC  | 1020 |
| ATGTCAAAAA | CCAGAAATCA | CTCCACTGCT  | TACCTTACAA | AATAGTGAAA  | TGATCTTAGA  | 1080 |
| GAACAAGGAC | AGCCATCACA | GA          |            |             |             | 1102 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Ser Met Ile Leu Gln Ile Ser

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Pro | Arg | Arg | Leu | Leu | Leu | Val | Ala | Ala | Cys | Phe | Ser | Leu | Cys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Pro | Leu | Leu | Ser | Ala | Arg | Thr | Arg | Ala | Arg | Arg | Pro | Glu | Ser | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Thr | Asn | Ala | Thr | Leu | Asp | Pro | Arg | Ser | Phe | Leu | Leu | Arg | Asn | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Asp | Lys | Tyr | Glu | Pro | Phe | Trp | Glu | Asp | Glu | Glu | Lys | Asn | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Leu | Thr | Glu | Tyr | Arg | Leu | Val | Ser | Ile | Asn | Lys | Ser | Ser | Pro | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Lys | Gln | Leu | Pro | Ala | Phe | Ile | Ser | Glu | Asp | Ala | Ser | Gly | Tyr | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Ser | Ser | Trp | Leu | Thr | Leu | Phe | Val | Pro | Ser | Val | Tyr | Thr | Gly | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Val | Val | Ser | Leu | Pro | Leu | Asn | Ile | Met | Ala | Ile | Val | Val | Phe | Ile |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Lys | Met | Lys | Val | Lys | Lys | Pro | Ala | Val | Val | Tyr | Met | Leu | His | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Thr | Ala | Asp | Val | Leu | Phe | Val | Ser | Val | Leu | Pro | Phe | Lys | Ile | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Tyr | Phe | Ser | Gly | Ser | Asp | Trp | Gln | Phe | Gly | Ser | Glu | Leu | Cys | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Val | Thr | Ala | Ala | Phe | Tyr | Cys | Asn | Met | Tyr | Ala | Ser | Ile | Leu | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Thr | Val | Ile | Ser | Ile | Asp | Arg | Phe | Leu | Ala | Val | Val | Tyr | Pro | Met |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Ser | Leu | Ser | Trp | Arg | Thr | Leu | Gly | Arg | Ala | Ser | Phe | Thr | Cys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Ile | Trp | Ala | Leu | Ala | Ile | Ala | Gly | Val | Val | Pro | Leu | Val | Leu | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Gln | Thr | Ile | Gln | Val | Pro | Gly | Leu | Asn | Ile | Thr | Thr | Cys | His | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Leu | Asn | Glu | Thr | Leu | Leu | Glu | Gly | Tyr | Tyr | Ala | Tyr | Tyr | Phe | Ser |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Phe | Ser | Ala | Val | Phe | Phe | Phe | Val | Pro | Leu | Ile | Ile | Ser | Thr | Val |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Tyr | Val | Ser | Ile | Ile | Arg | Cys | Leu | Ser | Ser | Ser | Ala | Val | Ala | Asn |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Ser | Lys | Lys | Ser | Arg | Ala | Leu | Phe | Leu | Ser | Ala | Ala | Val | Phe | Cys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | Phe | Ile | Ile | Cys | Phe | Gly | Pro | Thr | Asn | Val | Leu | Leu | Ile | Ala | His |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Tyr | Ser | Phe | Leu | Ser | His | Thr | Ser | Thr | Thr | Glu | Ala | Ala | Tyr | Phe | Ala |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Tyr | Leu | Leu | Cys | Val | Cys | Val | Ser | Ser | Ile | Ser | Ser | Cys | Ile | Asp | Pro |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Ile | Tyr | Tyr | Tyr | Ala | Ser | Ser | Glu | Cys | Gln | Arg | Tyr | Val | Tyr | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ile | Leu | Cys | Cys | Lys | Glu | Ser | Ser | Asp | Pro | Ser | Ser | Tyr | Asn | Ser | Ser |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gly | Gln | Leu | Met | Ala | Ser | Lys | Met | Asp | Thr | Cys | Ser | Ser | Asn | Leu | Asn |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asn | Ser | Ile | Tyr | Lys | Lys | Leu | Leu | Thr |     |     |     |     |     |     |     |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Pro | Ser | Ala | Ala | Trp | Leu | Leu | Gly | Ala | Ala | Ile | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Ala | Ser | Leu | Ser | Cys | Ser | Gly | Thr | Ile | Gln | Gly | Thr | Asn | Arg | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Lys | Gly | Arg | Ser | Leu | Ile | Gly | Lys | Val | Asp | Gly | Thr | Ser | His | Val |
|     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Thr | Gly | Lys | Gly | Val | Thr | Val | Glu | Thr | Val | Phe | Ser | Val | Asp | Glu | Phe |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Ala | Ser | Val | Leu | Thr | Gly | Lys | Leu | Thr | Thr | Val | Phe | Leu | Pro | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Tyr | Thr | Ile | Val | Phe | Val | Val | Gly | Leu | Pro | Ser | Asn | Gly | Met | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Trp | Val | Phe | Leu | Phe | Arg | Thr | Lys | Lys | Lys | His | Pro | Ala | Val | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Met | Ala | Asn | Leu | Ala | Leu | Ala | Asp | Leu | Leu | Ser | Val | Ile | Trp | Phe |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Lys | Ile | Ala | Tyr | His | Ile | His | Gly | Asn | Asn | Trp | Ile | Tyr | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Leu | Cys | Asn | Val | Leu | Ile | Gly | Phe | Phe | Tyr | Gly | Asn | Met | Tyr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Cys | Ser | Ile | Leu | Phe | Met | Thr | Cys | Leu | Ser | Val | Gln | Arg | Tyr | Trp | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Val | Asn | Pro | Met | Gly | His | Ser | Arg | Lys | Lys | Ala | Asn | Ile | Ala | Ile |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ile | Ser | Leu | Ala | Ile | Trp | Leu | Leu | Ile | Leu | Leu | Val | Thr | Ile | Pro |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Tyr | Val | Val | Lys | Gln | Thr | Ile | Phe | Ile | Pro | Ala | Leu | Asn | Ile | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Cys | His | Asp | Val | Leu | Pro | Glu | Gln | Leu | Leu | Val | Gly | Asp | Pro | Phe |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Ser | Leu | Ala | Ile | Gly | Val | Phe | Leu | Phe | Pro | Ala | Phe | Leu | Thr | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Ala | Tyr | Val | Leu | Met | Ile | Arg | Met | Leu | Arg | Ser | Ser | Ala | Met | Asp |
|     | 260 |     |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Asn | Ser | Glu | Lys | Lys | Arg | Lys | Arg | Ala | Ile | Lys | Leu | Ile | Val | Thr |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Leu | Ala | Met | Tyr | Leu | Ile | Cys | Phe | Thr | Pro | Ser | Asn | Leu | Leu | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Val | His | Tyr | Phe | Leu | Ile | Lys | Ser | Gln | Gly | Gln | Ser | His | Val | Tyr |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Leu | Tyr | Ile | Val | Ala | Leu | Cys | Leu | Ser | Thr | Leu | Asn | Ser | Cys | Ile |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Pro | Phe | Val | Tyr | Tyr | Phe | Val | Ser | His | Asp | Phe | Arg | Asp | His | Ala |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Asn | Ala | Leu | Leu | Cys | Arg | Ser | Val | Arg | Thr | Val | Lys | Gln | Met | Gln |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Val | Ser | Leu | Thr | Ser | Lys | Lys | His | Ser | Arg | Lys | Ser | Ser | Ser | Tyr | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ser | Ser | Ser | Thr | Thr | Val | Lys | Thr | Ser | Tyr |     |     |     |     |     |     |
| 385 |     |     |     |     | 390 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Phe | Glu | Glu | Ile | Pro | Glu | Glu | Tyr | Leu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...29
- (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24

- (A) NAME/KEY: Other
- (B) LOCATION: 22...27
- (D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTNTACATGC TNMACYTNGC NNTNGCNGA

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 6...21
- (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, and 21

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 24
- (D) OTHER INFORMATION: N=A or C or G or T at residue 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGATANACNA CNGCNADRWA NCKNTC

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Tyr Lys Asp Asp Asp

1

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
 1              5              10              15
Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr
      20              25              30
Lys Asp Asp Asp Asp Val Glu
      35
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Phe Glu Glu Phe Pro
 1              5
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Leu Thr Pro Lys
 1
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Phe Arg Gly Ala Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Phe Arg Gly Ala Pro Pro Asn Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu  
1 5 10 15  
Phe Pro Phe Ser Ala Leu Glu  
20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Pro Ile Lys Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu  
1 5 10 15  
Phe Pro Phe Ser Ala Leu Glu  
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Pro Ile Xaa Thr Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu  
1 5 10 15  
Glu Phe Pro Phe Ser Ala Leu Glu  
20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Xaa Pro Arg Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe  
1 5 10 15  
Pro Phe Ser Ala Leu Glu  
20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Pro Ile Lys  
1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Phe Arg Gly Ala Pro Pro Asn Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | His | Pro | Val | Ala | Gly | Ser | Gln | Asp | Ile | Lys | Met | Lys | Ile | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Ala | Ala | Gly | Leu | Leu | Phe | Leu | Pro | Val | Thr | Val | Cys | Gln | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ile | Asn | Val | Ser | Asp | Asn | Ser | Ala | Lys | Pro | Thr | Leu | Thr | Ile | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Asn | Gly | Gly | Pro | Gln | Asn | Thr | Phe | Glu | Glu | Phe | Pro | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Ile | Glu | Gly | Trp | Thr | Gly | Ala | Thr | Thr | Thr | Ile | Lys | Ala | Glu | Cys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Glu | Asp | Ser | Ile | Ser | Thr | Leu | His | Val | Asn | Asn | Ala | Thr | Ile | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Leu | Arg | Ser | Ser | Leu | Ser | Thr | Gln | Val | Ile | Pro | Ala | Ile | Tyr | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Leu | Leu | Phe | Val | Val | Gly | Val | Pro | Ser | Asn | Ile | Val | Thr | Leu | Trp | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Leu | Arg | Thr | Lys | Ser | Ile | Ser | Leu | Val | Ile | Phe | His | Thr | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Leu | Ala | Ile | Ala | Asp | Leu | Leu | Phe | Cys | Val | Thr | Leu | Pro | Phe | Lys | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Tyr | His | Leu | Asn | Gly | Asn | Asn | Trp | Val | Phe | Gly | Glu | Val | Met | Cys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Ile | Thr | Thr | Val | Val | Phe | Tyr | Gly | Asn | Met | Tyr | Cys | Ala | Ile | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Ile | Leu | Thr | Cys | Met | Gly | Ile | Asn | Arg | Tyr | Leu | Ala | Thr | Ala | His | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Thr | Tyr | Gln | Lys | Leu | Pro | Lys | Arg | Ser | Phe | Ser | Leu | Leu | Met | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ile | Val | Trp | Val | Met | Val | Phe | Leu | Tyr | Met | Leu | Pro | Phe | Val | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Lys | Gln | Glu | Tyr | His | Leu | Val | His | Ser | Glu | Ile | Thr | Thr | Cys | His |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Val | Val | Asp | Ala | Cys | Glu | Ser | Pro | Ser | Ser | Phe | Arg | Phe | Tyr | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Val | Ser | Leu | Ala | Phe | Phe | Gly | Phe | Leu | Ile | Pro | Phe | Val | Ile | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Phe | Cys | Tyr | Thr | Thr | Leu | Ile | His | Lys | Leu | Lys | Ser | Lys | Asp | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Trp | Leu | Gly | Tyr | Ile | Lys | Ala | Val | Leu | Leu | Ile | Leu | Val | Ile | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Ile | Cys | Phe | Ala | Pro | Thr | Asn | Ile | Ile | Leu | Val | Ile | His | His | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Tyr | Tyr | Tyr | His | Asn | Thr | Asp | Ser | Leu | Tyr | Phe | Met | Tyr | Leu | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Leu | Cys | Leu | Gly | Ser | Leu | Asn | Ser | Cys | Leu | Asp | Pro | Phe | Leu | Tyr |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Phe | Val | Met | Ser | Lys | Val | Val | Asp | Gln | Leu | Asn | Pro |     |     |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

Ser Ala Met Ala Arg Pro Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Arg Pro Arg Arg Asp Ile Trp Glu Asp Ile His Ala Trp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Met | Ile | Leu | Gln | Ile | Ser | Xaa | Arg | Leu | Arg | Asp | Gly | Thr | Gln | 1   | 5   | 10  | 15  |
| Val | Ile | Lys | Met | Lys | Ala | Leu | Ile | Phe | Ala | Ala | Ala | Gly | Leu | Leu | Leu | 20  | 25  | 30  |     |
| Leu | Leu | Pro | Thr | Phe | Cys | Gln | Ser | Gly | Met | Glu | Asn | Asp | Thr | Asn | Asn | 35  | 40  | 45  |     |
| Leu | Ala | Lys | Pro | Thr | Leu | Pro | Ile | Lys | Thr | Phe | Arg | Gly | Ala | Pro | Pro | 50  | 55  | 60  |     |
| Asn | Ser | Phe | Glu | Glu | Phe | Pro | Phe | Ser | Ala | Leu | Glu | Gly | Trp | Thr | Gly | 65  | 70  | 75  | 80  |
| Ala | Thr | Ile | Thr | Val | Lys | Ile | Lys | Cys | Pro | Glu | Glu | Ser | Ala | Ser | His | 85  | 90  | 95  |     |
| Leu | His | Val | Lys | Asn | Ala | Thr | Met | Gly | Tyr | Leu | Thr | Ser | Ser | Leu | Ser | 100 | 105 | 110 |     |
| Thr | Lys | Leu | Ile | Pro | Ala | Ile | Tyr | Leu | Leu | Val | Phe | Val | Val | Gly | Val | 115 | 120 | 125 |     |
| Pro | Ala | Asn | Ala | Val | Thr | Leu | Trp | Met | Leu | Phe | Phe | Arg | Thr | Arg | Ser | 130 | 135 | 140 |     |
| Ile | Cys | Thr | Thr | Val | Phe | Tyr | Thr | Asn | Leu | Ala | Ile | Ala | Asp | Phe | Leu | 145 | 150 | 155 | 160 |
| Phe | Cys | Val | Thr | Leu | Pro | Phe | Lys | Ile | Ala | Tyr | His | Leu | Asn | Gly | Asn | 165 | 170 | 175 |     |
| Asn | Trp | Val | Phe | Gly | Glu | Val | Leu | Cys | Arg | Ala | Thr | Thr | Val | Ile | Phe | 180 | 185 | 190 |     |
| Tyr | Gly | Asn | Met | Tyr | Cys | Ser | Ile | Leu | Leu | Leu | Ala | Cys | Ile | Ser | Ile | 195 | 200 | 205 |     |
| Asn | Arg | Tyr | Leu | Ala | Ile | Val | His | Pro | Phe | Thr | Tyr | Arg | Gly | Leu | Pro | 210 | 215 | 220 |     |
| Lys | His | Thr | Tyr | Ala | Leu | Val | Thr | Cys | Gly | Leu | Val | Trp | Ala | Thr | Val | 225 | 230 | 235 | 240 |
| Phe | Leu | Tyr | Met | Leu | Pro | Phe | Phe | Ile | Leu | Lys | Gln | Glu | Tyr | Tyr | Leu | 245 | 250 | 255 |     |
| Val | Gln | Pro | Asp | Ile | Thr | Thr | Cys | His | Asp | Val | His | Asn | Thr | Cys | Glu | 260 | 265 | 270 |     |
| Ser | Ser | Ser | Pro | Phe | Gln | Leu | Tyr | Tyr | Phe | Ile | Ser | Leu | Ala | Phe | Phe | 275 | 280 | 285 |     |
| Gly | Phe | Leu | Ile | Pro | Phe | Val | Leu | Ile | Ile | Tyr | Cys | Tyr | Ala | Ala | Ile |     |     |     |     |

290                      295                      300  
 Ile Arg Thr Leu Asn Ala Tyr Asp His Arg Trp Leu Trp Tyr Val Lys  
 305                      310                      315                      320  
 Ala Ser Leu Leu Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Ser  
                     325                      330                      335  
 Asn Ile Ile Leu Ile Ile His His Ala Asn Tyr Tyr Tyr Asn Asn Thr  
                     340                      345                      350  
 Asp Gly Leu Tyr Phe Ile Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu  
                     355                      360                      365  
 Asn Ser Cys Leu Asp Pro Phe Leu Tyr Phe Leu Met Ser Lys Thr Arg  
                     370                      375                      380  
 Asn His Ser Thr Ala Tyr Leu Thr Lys  
                     385                      390

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

Asn Asp Leu Arg Glu Gln Gly Gln Pro Ser Gln Arg Thr  
 1                      5                      10